SEQUENCE LISTING

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Saito, Mikiyoshi
Orita, Tetsuro

<120> METHODS OF SCREENING FOR MODIFIED ANTIBODIES WITH AGONISTIC ACTIVITIES

<130> 14875-163US1

<150> PCT/JP2004/18499
<151> 2004-12-10

<150> JP 2003-415733
<151> 2003-12-12

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<170> PatentIn version 3.1

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1               5                   10                  15

gtc cac tcc cag gtt cag ctg cag cag tct gga cct gag ttg gtg aag       96
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30

cct ggg gcc tca gtg aag att tcc tgc aag gct tct ggc tat gca ttc      144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
        35                  40                  45

agt agt tcc tgg atg aac tgg gtg aag cag agg cct gga aag ggt ctt      192
Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu
    50                  55                  60

gag tgg att gga cgg att tat cct gga gat gga gat act aac tac aat      240
Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn
65                  70                  75                  80

ggg aag ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc      288
Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95

acg gcc tac ata caa ctc agc agc cta aca tct gag gac tct gcg gtc      336
Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

tac ttc tgt gca aga ggg tat gct gac tac tcc ttt gct tac tgg ggc      384
Tyr Phe Cys Ala Arg Gly Tyr Ala Asp Tyr Ser Phe Ala Tyr Trp Gly
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caa ggg act ctg gtc act gtc tct gca                                  411
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            20                  25                  30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
        35                  40                  45

Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn
65                  70                  75                  80
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Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
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1               5                   10                  15

gga gcc att ggg gat att gtg atg act cag gct gca ccc tct gta cct       96
Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro
            20                  25                  30

gtc act cct gga gag tca gta tcc atc tcc tgc agg tct agt aag agt      144
Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser
        35                  40                  45

ctc ctg cat agt aat ggc aac act tac ttg tat tgg ttc ctg cag agg      192
Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg
    50                  55                  60

cca ggc cag tct cct cag ctc ctg ata tat cgg atg tcc aac ctt gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala
65                  70                  75                  80

tca gga gtc cca gac agg ttc agt ggc agt ggg tca gga act gct ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe
                85                  90                  95

aca ctg aga atc agt aga gtg gag gct gag gat gtg ggt gtt tat tac      336
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110

tgt atg caa cat cta gaa tat ccg tat acg ttc gga tcg ggg acc aag      384
Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Ser Gly Thr Lys
        115                 120                 125

ctg gaa ata aaa                                                     396
Leu Glu Ile Lys
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35 40 45

Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe
85 90 95

Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Ser Gly Thr Lys
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<212> DNA
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cttttatttc agcttggtc c 81